AMENDMENTS TO THE CLAIMS:

Please amend the claims as follows:

1. (Currently Amended) A method for determination of amounts or relative proportions of more than one individual ~~polynucleotide~~ ribopolynucleotide sequence or subgroups thereof in a sample comprising a ~~polynucleotide~~ mixture of target ribopolynucleotide sequences using a quantitative affinity aided solution hybridization in combination with size- or mass-based fractionation for obtaining resolution, ~~characterized in that~~ wherein the method comprises the consecutive steps of:

(a) providing, one or more ~~organized~~ pools with ~~a preset optional number of~~ more than one soluble polynucleotide probe~~s~~, wherein each probe in said pool is ~~being~~ complementary to an individual target ~~ribopolynucleotides~~ ribopolynucleotide sequence in the sample, being present in a molar excess as compared to the ~~analyte polynucleotide~~ target ribopolynucleotide sequences, and ~~having~~ has approximately the same number of hybridizing nucleotides, which are complementary to said target ribopolynucleotide sequences, wherein approximately the same number of nucleotides means that the polynucleotide probes are not distinguishable from each other in size- or mass-based separation, fractionation and recording and are made distinguishable by providing said polynucleotide probes with one or more resolution enabling tags, which tags are oligonucleotide residues, which change the mass or size of the polynuclotide probes and provide ~~the polynucleotide probes~~ them with different mobilities in fractionation, separation or recording systems without disturbing the hybridization or capturing reaction, wherein each pool of polynucleotide probes are placed in their own vessels;

(b) providing ~~the analyte polynucleotide~~ a mixture of affinity tagged target ribopolynucleotide sequences by contacting the sample comprising the ~~isolated from a sample comprising a~~ mixture of target ribopolynucleotide sequences with at least one affinity tag; and thereafter

(c) performing steps (i) and (ii) simultaneously, or sequentially; in the order (i) and (ii), wherein ~~the~~ steps (i) and (ii) ~~comprises~~ comprise: (i) allowing a hybridization reaction to take place between the molar excess of ~~soluble~~ polynucleotide probes from step (a) and the ~~analyte~~ affinity tagged target ribopolynucleotide sequences from step

(b) leading to ~~a quantitative~~ formation of ~~soluble~~ hybrids; (ii) providing captured hybrids by recovering the hybrids, ~~which have been quantitatively formed in step (i) by capturing said hybrids quantitatively~~ on a separation aiding tool provided with ~~the~~ an affinity pair of the affinity tag of the ~~analyte polynucleotide~~ target ribopolynucleotide sequences;

(d) ~~quantitatively releasing the~~ providing released polynucleotide probes by eluting the polynucleotide probes in an unmodified form from the captured hybrids ~~captured to separation aiding too~~, wherein said released polynucleotide probes are provided with tracer tags in step (a) or are tracer tagged after release in step (d) or during or after amplifiecation after the release in step (d);

(e) separating the released polynucleotide probes by electrophoretic or chromatographic techniques or mass spectrometry and recording the amount or relative proportions of distinguishable polynucleotide probes, the amount of which corresponds to the amount of complementary target ribopolynucleotide sequences in the mixture of ~~analyte~~ target ribopolynucleotide sequences in the sample.

2. (Currently Amended) The method according to claim 1, ~~characterized in that~~ wherein for the determination of ~~dynamic~~ variations in the amounts or relative proportions of polynucleotide transcripts or their subgroups in an individual organism, the soluble polynucleotide probes are designed from species or group-specific ribopolynucleotide sequences hybridizing with selected ~~more or less~~ conserved or hypervariable regions from intragenomic sequences specific for subgroups, species, subspecies of transcripts expressed in the organism.

3. (Currently Amended) The method according to claim 2, ~~characterized in that~~ wherein the ~~analyte polynucleotide~~ target ribopolynucleotide sequences ~~isolated~~ from the sample comprising ~~the~~ a mixed target population ~~is~~ are messenger RNA (mRNA).

4. (Currently Amended) The method according to claim 1, ~~characterized in that~~ wherein for the determination of ~~dynamic~~ variations in the amounts or relative proportions of ribopolynucleotide sequences representing individual organisms or subpopulations thereof in a target population, the ~~soluble deoxyribopolynucleotide~~

polynucleotide probes are designed from species or group-specific ribopolynucleotide sequences hybridizing with a selected ~~more or less~~ conserved or hypervariable region from intragenomic sequences specific for and/or representing different phylogenetic levels allowing the identification of subgroups, species, subspecies within ~~the~~ a mixed target population.

5. (Currently Amended) The method according to claim 4, ~~characterized in that~~ wherein the target ribopolynucleotide sequences ~~analytes~~ ~~isolated~~ from the sample comprising the mixed target population ~~comprise~~ are ribosomal RNA.

6-9. (Cancelled)

10. (Currently Amended) The method according to claim 1, ~~7, characterized in that~~ wherein the ~~resolution enabling tags which additionally may as acts a~~ be tracer tags ~~tag is selected from a group consisting of labels~~ are recordable by fluorescence, ~~luminescence, infrared absorption, electromagnetic properties, and radioactivity, and enzymatic activity~~.

11. (Currently Amended) The method according to claim 1, ~~characterized in that~~ wherein more than five ~~the preset optional number of~~ ~~soluble~~ polynucleotide probes are in the pool ~~is more than one preferably more than five, most preferably more than ten~~.

12. (Currently Amended) The method according to claim 1, ~~characterized in that~~ wherein the amount of the individual, ~~quantitatively~~ captured and released polynucleotide probes is recorded with a fully or partly ~~automized~~ automatic recording system, ~~which is selected based on the applied resolution enabling tags~~.

13. (Currently Amended) The method according to claim 12, ~~characterized in that~~ wherein the ~~recording system is selected based on resolution enabling tags and comprises mass spectrometry,~~ electrophoretic or chromatographic techniques are capillary electrophoresis.

14. (Currently Amended) The method according to claim 1 ~~any of claims 1-13, characterized in that~~ wherein the amount of ~~the quantitatively recovered primer tagged~~ polynucleotide probes, wherein the resolution enabling tags are oligonucleotide residues acting as primers, are released and subsequently amplified and ~~optionally~~ tracer tagged ~~before~~ during or after the ~~PCR-reaction~~ amplification and thereafter recorded ~~with a recording system selected based on the resolution enabling tags~~.

15. (Currently Amended) The method according to claim 14, ~~characterized in that~~ wherein the primers comprise specific and universal parts.

16. (Currently Amended) The method according to claim 1, ~~characterized in that~~ wherein the polynucleotide probes are selected from the group consisting of stable DNA fragments, synthetic or recombinant polynucleotide sequences, and ~~or~~ modified polynucleotide sequences.

17. (Currently Amended) The method according to claim 1, ~~characterized in that~~ wherein a comparative, quantitative assessment of variations in the amounts of individual target ribopolynucleotide sequences or organisms and subgroups thereof in a population or mixture of target ribopolynucleotide ~~polynucleotide~~ sequences is carried out by providing ~~a set~~ sets of ~~multiple~~ test kits, at least one test kit for each sample to be compared, wherein each of said test kits are provided with ~~one or more~~ identical ~~organized~~ pools comprising more than one ~~with a preset optional number of soluble~~ polynucleotide probe ~~probes, each probe being DNA complementary to an individual target ribopolynucleotide sequence in the sample, being present in a molar excess as compared to the target polynucleotide samples, and having approximately the same number of hybridizing nucleotides and having an indistinguishable number of hybridizing nucleotides, probes are made distinguishable by providing each polynucleotide probe with one or more resolution enabling tags, which tags change the size or mass and thereby provide the polynucleotide probes with different mobilities in the fractionation, separation or recording systems without disturbing the hybridization or capturing~~

~~reaction, each pool of polynucleotides probes being placed in an organized manner in their own vessels, which are separate or joined together~~.

18. (Currently Amended) The method according to claim 17, ~~the individual test kits, characterized in that~~ wherein ~~the resolution enabling tag is not a tracer tag, a multiple~~ each set of test kits is provided with a tracer tag, which is ~~tracer tags each being~~ distinguishable ~~from the other~~ by the emitted signal.

19. (Currently Amended) The ~~use in any~~ method according to claim 1, ~~claims 1-18 of a test kit, characterized in that~~ wherein the steps of the method are performed on a test kit, which comprises one or more ~~organized~~ pools, with ~~a preset optional number of~~ more than one soluble polynucleotide probe ~~probes, each probe being complementary to an individual target ribopolynucleotide sequence in the sample, being present in a molar excess as compared to the analyte in the samples, and having approximately the same number of hybridizing nucleotides, are made distinguishable by providing each polynucleotide probes with one or more resolution enabling tags, which change the size or mass and thereby provide the polynucleotide probes with different mobilities in the fractionation, separation or recording systems without disturbing the hybridization or capturing reaction, each pool of polynucleotides probes being placed in an organized manner in their own vessels, which are separate or joined together~~.

20-29 (Cancelled)

30. (Currently Amended) The ~~use~~ method according to claim 1, ~~19, characterized in that~~ wherein the ~~soluble~~ pools ~~of~~ comprising polynucleotide probes are placed in wells on a microtiter plate.

31-35. (Cancelled)

36. (New) The method according to claim 17 for assessing hygienic conditions and epidemiologic situations, effects of external stimuli or treatment modalities on a

microbial population, wherein a comparative assessment of variations in the amounts or relative proportions of more than one individual target ribopolynucleotide sequence or subgroups thereof in a sample from a population are determined by providing a set of identical test kits for each sample to be compared, wherein the samples are obtained before and after applying the external stimulus or treatment.

37. (New) The method according to claim 1, wherein the number of soluble polynucleotide probes in the pool is more than ten.

38. (New) The method according to claim 1, wherein the polynucleotide probes are tracer tagged in step (a).

39. (New) The method according to claim 1, wherein the polynucleotide probes are tracer tagged after the release in step (d).

40. (New) The method according to claim 1, wherein the released polynucleotide probes in step (d) are amplified and tracer tagged during or after amplification.

41. (New) The method according to claim 1, wherein the tracer tag is a fluorophor.